

Amendments to the Specification

Please replace the paragraph at page 15, lines 25 through 29 with the following amended paragraph:

Based on the above methods, two-dimensional electrophoresis has already been performed for many proteomes. The analytical results obtained by amino acid sequencing and peptide mass fingerprinting methods performed on isolated protein spots have been ~~recorded along~~ recorded along with coordinate information, and stored in databases such as SWISS-2DPAGE® (<http://expasy.heuge.ch/ch2d/>), etc.

Please replace the paragraph at page 24, lines 4 through 12 with the following amended paragraph:

On the other hand, compared with labor-intensive amino acid sequencing, peptide mass-fingerprinting methods can more speedily provide a variety of information useful for protein identification. Mass patterns (i.e. fingerprints) of the protease-digested fragments are obtained by using a set protease to digest the proteins contained in the spots separated as a result of two-dimensional electrophoresis, and then analyzing the fragments thus obtained using a mass spectrogram. Proteins can be identified based on these peptide mass fingerprints since they are information highly unique to individual proteins, and databases which accumulate such data, such as ProteinProspector PROTEINPROSPECTOR® (<http://prospector.ucsf.edu/>), can be utilized on the Internet.